

CLAIMS

1. Peptide comprising essentially the peptide sequence of formula (I),

5 Xaa-Cys-Xab-Cys-Xac-Cys-Xad-Cys-Xae-Cys-Xaf-Cys-Xag
(I)

in which:

Xaa is -NH₂ or a peptide residue comprising 10 from 1 to 10 amino acids, preferably from 1 to 6 amino acids,

Xab is a peptide residue comprising from 1 to 10 amino acids, preferably 10,

15 Xac is a peptide residue of 3 amino acids,

Xad is a peptide residue comprising from 1 to 9 amino acids, preferably 9,

7 Xae is a peptide residue comprising from 1 to 7 amino acids, preferably 7,

20 Xaf is a peptide residue of 1 amino acid, and

Xag is -OH or a peptide residue comprising from 1 to 5 amino acids, preferably 1 or 2 amino acids.

2. Peptide according to claim 1,

characterized in that

Xaa comprises at least one basic amino acid, and/or

25 Xad comprises at least one basic amino acid.

3. Peptide according to claim 2,
characterized in that Xad comprises 1, 2, 3 or 4 basic
amino acids.

claim 2

4. Peptide according to ~~either of claims 2~~
5 and 3, characterized in that the basic amino acids are
chosen from lysine, arginine or homoarginine.

claim 1

5. Peptide according to ~~one of claims 1 to~~
A 4, characterized in that Xad represents the following
peptide sequence -Lys-Xad'-Xad"-Gly-His-, in which Xad'
10 represents a peptide residue of 1 basic amino acid and
Xad" represents a peptide residue comprising from 0 to
5 amino acids, preferably 5.

claim 1

A SUB C2) 6. Peptide according to ~~one of claims 1 to~~
5, characterized in that Xad represents the following
15 peptide sequence -Lys-Arg-Arg-Gly-Tyr-Lys-Gly-Gly-His-.

7. Peptide according to one of claims 1 to
6, characterized in that Xac comprises at least one
acidic amino acid, preferably 1.

claim 1

A 8. Peptide according to ~~one of claims 1 to~~
20 7, characterized in that Xac represents the following
peptide sequence -Asn-Xac'-Xac"-, in which Xac'
represents a peptide residue of 1 amino acid, and Xac"
represents a peptide residue of 1 acidic amino acid.

claim 7

A 25 and 8, characterized in that the acidic amino acids are
chosen from glutamic acid (Glu) or aspartic acid (Asp).

claim 1

10. Peptide according to ~~one of claims 1 to 10~~, characterized in that Xac represents the following peptide sequence -Asn-Gly-Glu-.

claim 1

11. Peptide according to ~~one of claims 1 to 10~~, characterized in that

Xaa represents the following peptide sequence Xaa'-Gly-Xaa"- in which Xaa' represents NH₂ or a peptide residue comprising 1 to 9 amino acids, preferably 1 to 5 amino acids, and Xaa" represents a peptide residue comprising

10 at least one amino acid, preferably chosen from Leu, Ile, Val, Pro, Ser or Thr, and/or

Xab represents the following peptide sequence -Val-Xab'-Asp-, in which Xab' represents a peptide residue comprising from 0 to 8 amino acids, preferably 8,

15 and/or

Xae represents the following peptide sequence -Gly-Xae'-Asn-, in which Xae' represents a peptide residue comprising from 0 to 5 amino acids, preferably 5, and/or

20 Xaf represents one of the following amino acids Trp, Phe, Leu, Ile or Val and/or

Xag represents the following peptide sequence -Glu-Xag' in which Xag' represents OH or a variable residue having a sequence comprising from 1 to 4 amino acids,

25 preferably 1 amino acid.

claim 1

12. Peptide according to ~~one of claims 1 to 11~~, characterized in that

Subc4)

Xaa represents the following peptide sequence NH₂-Asp-Lys-Leu-Ile-Gly-Ser-, and/or

Xab represents the following peptide sequence -Val-Trp-Gly-Ala-Val-Asn-Tyr-Thr-Ser-Asp-, and/or

5 Xae represents the following peptide sequence -Gly-Ser-Phe-Ala-Asn-Val-Asn-, and/or

Xaf represents the following amino acid -Trp- and/or

Xag represents the following peptide sequence -Glu-Thr-OH.

claim 1

10 13. Peptide according to one of claims 1 to
12, characterized in that it is represented by the
identifier No. 2 (SEQ ID NO 2).

claim 1

14. Peptide according to one of claims 1 to
13, characterized in that it comprises at either of its
15 ends, or at both ends, peptide residues necessary for
its expression and targeting in a host organism.

claim 1

15. Peptide according to one of claims 1 to
14, characterized in that the cysteine residues of the
peptide of formula (I) form at least one intramolecular
20 disulphide bridge.

16. Peptide according to claim 15,
characterized in that it comprises 3 disulphide bridges
established between the cysteine residues 1 and 4, 2
and 5, and 3 and 6.

25 17. "Peptide-heliomicine" fusion peptide,
characterized in that the heliomicine is a peptide
defined according to one of claims 1 to 16.

claim 1

18. Fusion peptide according to claim 17,
characterized in that the peptide fused with
heliomicine is a signal peptide or a transit peptide.

19. Fusion peptide according to claim 18,
5 characterized in that the transit peptide is the signal
peptide of the tobacco PR-1 α gene or the precursor of
factor Mat alpha 1 or the signal peptide of the maize
polygalacturonase PG1 gene.

20. Fusion peptide according to claim 19,
10 characterized in that it is represented by the sequence
identifier No. 1 (SEQ ID NO 1), by the sequence
identifier No. 3 (SEQ ID NO 3), or by the sequence
identifier No. 18 (SEQ ID NO 18).

21. As a medicament, the peptide according
15 to one of claims 1 to 20.

22. Composition, characterized in that it
comprises the peptide according to ^{Claim 1}
~~one of claims 1 to~~
20 and an appropriate vehicle.

23. Nucleic acid fragment, characterized in
20 that it comprises a nucleic acid sequence encoding a
peptide according to ^{Claim 1}
~~one of claims 1 to 20~~.

24. Nucleic acid fragment according to claim
23, characterized in that it is a nucleotide sequence
of the DNA type.

25. Nucleic acid fragment according to claim
24, characterized in that the nucleotide sequence of
the DNA type comprises the DNA sequence described by
bases 16 to 147 of the sequence identifier No. 1 (SEQ
5 ID NO 1), by the sequence identifier No. 2 (SEQ ID NO
2), by bases 3 to 224 of the sequence identifier No. 3
(SEQ ID NO 3), or by bases 7 to 205 of the sequence
identifier No. 18 (SEQ ID NO 18), a homologous sequence
or a sequence complementary to the said sequence.

10 26. Chimeric gene comprising a coding
sequence as well as heterologous regulatory elements at
the 5' and 3' positions capable of functioning in a
host organism, in particular plants, characterized in
that the coding sequence comprises at least one DNA
15 fragment as defined in claims ~~23 to 25~~.

A
27. Chimeric gene according to claim 26,
characterized in that the host organism is a
microorganism.

28. Chimeric gene according to claim 26,
20 characterized in that the host organism is chosen from
plant cells and plants.

29. Cloning or expression vector for the
transformation of a host organism, characterized in
that it comprises at least one replication origin and
25 at least one chimeric gene as defined in claims ~~26 to~~
~~28~~.

A
30. Transformed host organisms, characterized in that they contain a nucleic acid fragment according to claims 23 to 25, or a chimeric gene according to claims 26 to 28.

5 31. Transformed host organism according to claim 30, characterized in that it includes microorganisms, plant cells or plants.

10 32. Transformed host organism according to claim 30, characterized in that it is a plant containing transformed cells.

33. Host organism according to claim 32, characterized in that the plant is regenerated from transformed cells.

15 34. Transformed host organism according to claim 30, characterized in that the microorganism is chosen from bacteria, in particular *E. coli*, yeasts, in particular of the genera *Saccharomyces* or *Kluyveromyces*, *Pichia*, fungi, in particular *Aspergillus*, or baculoviruses.

20 35. Transformed plant cell, characterized in that it contains a nucleic acid fragment according to claims 23 to 25 or a chimeric gene according to claims 26 to 28.

25 36. Transformed plant, characterized in that it comprises at least one transformed plant cell according to claim 35.

37. Transformed plant according to claim 36,
characterized in that it is resistant to diseases
caused by *Cercospora*, in particular *Cercospora*
beticola, *Cladosporium*, in particular *Cladosporium*
5 *herbarum*, *Fusarium*, in particular *Fusarium culmorum* or
Fusarium graminearum, or by *Phytophthora*, in particular
Phytophthora cinnamomi.

38. Transformed plant, characterized in that
it is derived from the cultivation and/or crossing of
10 the plants according to ^{Claim 36} either of claims 36 and 37.

A 39. Seeds of transformed plants according to ^{Claim 36}
~~one of claims 36 to 38~~.

40. Method of transforming host organisms,
in particular plant cells or plants, characterized in
15 that at least one nucleic acid fragment according to
claims ~~/ 23 to 25 or a chimeric gene according to one of~~
~~claims 26 to 28~~ is inserted into the said host
organism.

41. Method according to claim 40,
20 characterized in that the host organism is a plant cell
or a plant.

42. Method according to claim 41,
characterized in that a plant is regenerated from the
plant cell or from the transformed plant.

43. Method of cultivating transformed plants
according to ~~one of claims 36 to 38~~, characterized in
that it consists in planting the seeds of the said
transformed plants in a plot of a field appropriate for
5 cultivating the said plants, in applying to the said
plot of the said field an agrochemical composition,
without substantially affecting the said seeds or the
said transformed plants, then in harvesting the
cultivated plants when they arrive at the desired
10 maturity and optionally in separating the seeds from
the harvested plants.

44. Method of cultivation according to claim
~~43~~
~~33~~, characterized in that the agrochemical composition
comprises at least one active product having at least
15 one fungicidal and/or bactericidal activity.

45. Method of cultivation according to claim
44, characterized in that the active product exhibits
an activity which is complementary to that of the
peptide according to one of claims 1 to 20.

20 46. Method of preparing heliomicine defined
according to ~~one of claims 1 to 20~~, characterized in
that it comprises the steps of culturing a transformed
organism ~~according to one of claims 30 to 34~~ in an
appropriate culture medium, followed by the extraction
25 and total or partial purification of the heliomicine
obtained.